

**Amendments to the Specification**

Please replace the paragraph beginning at page 4, line 11, with the following redlined paragraph.

~~Figure 11 depicts Figures 11A and 11B depict~~ the comparison of the predicted amino acid sequences of the BVH-3 open reading frames from WU2, RX1, JNR.7/87, SP64, P4241 and A66 S. pneumoniae strains by using the program Clustal W from MacVector sequence analysis software (version 6.5). Underneath the alignment, there is a consensus line where \* and . characters indicate identical and similar amino acid residues, respectively.

Please replace the paragraph beginning at page 4, line 19, with the following redlined paragraph.

~~Figure 12 depicts Figures 12A-12D depict~~ the comparison of the predicted amino acid sequences of the BVH-11 open reading frames from WU2, RX1, JNR.7/87, SP64, P4241 and A66 and SP63 S. pneumoniae strains by using the program Clustal W from MacVector sequence analysis software (version 6.5). Underneath the alignment, there is a consensus line where \* and . characters indicate identical and similar amino acid residues, respectively.

Please replace the paragraph beginning at page 5, line 1, with the following redlined paragraph.

~~Figure 14~~ Figures 14A and 14B is-present a DNA sequence containing the complete BVH-3 gene (open reading frame "ORF" at nucleotides 1777 to 4896); **SEQ ID No: 11.**

Please replace the paragraph beginning at page 7, line 19, with the following redlined paragraph.

~~Figure 41~~ Figures 41A and 41B is-present the DNA sequence of NEW12 gene; **SEQ ID No: 76.**